Batch 1641

**CRF E[illegible]s Corrected by th STIC System [illegible]ranch**

**Serial Number:** 08/908,453

CRF Processing Date: 10/22/98 #9
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: ENTERED

☑ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☑ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

_____

***Examin r: Th abov corrections must b communicated to th applicant in the first Offic Action. DO NOT send a copy of this form.**

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/908,453*

DATE: 10/22/98
TIME: 09:36:26

*INPUT SET: S29199.raw*

**This Raw Listing contains the General Information Section and up to the first 5 pages.**



SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Ruvkun, Gary
Morris, Jason
Tissenbaum, Heidi

(ii) TITLE OF THE INVENTION: AGE-1 POLYPEPTIDES AND RELATED MOLECULES AND METHODS

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US97/13914
(B) FILING DATE: 07-AUG-1997

(A) APPLICATION NUMBER: 60/023,382
(B) FILING DATE: 07-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Elbing, Karen L
(B) REGISTRATION NUMBER: 35,238
(C) REFERENCE/DOCKET NUMBER: 08472/704WO2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-428-0200
(B) TELEFAX: 617-428-7045
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met His Val Asn Ile Leu His Pro Gln Leu Gln Thr Met Val Glu Gln
 1               5                  10                  15
Trp Gln Met Arg Glu Arg Pro Ser Leu Glu Thr Glu Asn Gly Lys Gly
            20                  25                  30
Ser Leu Leu Leu Glu Asn Glu Gly Val Ala Asp Ile Ile Thr Met Cys
        35                  40                  45
Pro Phe Gly Glu Val Ile Ser Val Val Phe Pro Trp Phe Leu Ala Asn
    50                  55                  60
Val Arg Thr Ser Leu Glu Ile Lys Leu Ser Asp Phe Lys His Gln Leu
65                  70                  75                  80
Phe Glu Leu Ile Ala Pro Met Lys Trp Gly Thr Tyr Ser Val Lys Pro
                85                  90                  95
Gln Asp Tyr Val Phe Arg Gln Leu Asn Asn Phe Gly Glu Ile Glu Val
            100                 105                 110
Ile Phe Asn Asp Asp Gln Pro Leu Ser Lys Leu Glu Leu His Gly Thr
        115                 120                 125
Phe Pro Met Leu Phe Leu Tyr Gln Pro Asp Gly Ile Asn Arg Asp Lys
    130                 135                 140
Glu Leu Met Ser Asp Ile Ser His Cys Leu Gly Tyr Ser Leu Asp Lys
145                 150                 155                 160
Leu Glu Glu Ser Leu Asp Glu Glu Leu Arg Gln Phe Arg Ala Ser Leu
                165                 170                 175
Trp Ala Arg Thr Lys Lys Thr Cys Leu Thr Arg Gly Leu Glu Gly Thr
            180                 185                 190
Ser His Tyr Ala Phe Pro Glu Glu Gln Tyr Leu Cys Val Gly Glu Ser
        195                 200                 205
Cys Pro Lys Asp Leu Glu Ser Lys Val Lys Ala Ala Lys Leu Ser Tyr
    210                 215                 220
Gln Met Phe Trp Arg Lys Arg Lys Ala Glu Ile Asn Gly Val Cys Glu
225                 230                 235                 240
Lys Met Met Lys Ile Gln Ile Glu Phe Asn Pro Asn Glu Thr Pro Lys
                245                 250                 255
Ser Leu Leu His Thr Phe Leu Tyr Glu Met Arg Lys Leu Asp Val Tyr
            260                 265                 270
Asp Thr Asp Asp Pro Ala Asp Glu Gly Trp Phe Leu Gln Leu Ala Gly
        275                 280                 285
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100  Arg Thr Thr Phe Val Thr Asn Pro Asp Val Lys Leu Thr Ser Tyr Asp
101      290                 295                 300
102  Gly Val Arg Ser Glu Leu Glu Ser Tyr Arg Cys Pro Gly Phe Val Val
103  305                 310                 315                 320
104  Arg Arg Gln Ser Leu Val Leu Lys Asp Tyr Cys Arg Pro Lys Pro Leu
105                  325                 330                 335
106  Tyr Glu Pro His Tyr Val Arg Ala His Glu Arg Lys Leu Ala Leu Asp
107              340                 345                 350
108  Val Leu Ser Val Ser Ile Asp Ser Thr Pro Lys Gln Ser Lys Asn Ser
109          355                 360                 365
110  Asp Met Val Met Thr Asp Phe Arg Pro Thr Ala Ser Leu Lys Gln Val
111      370                 375                 380
112  Ser Leu Trp Asp Leu Asp Ala Asn Leu Met Ile Arg Pro Val Asn Ile
113  385                 390                 395                 400
114  Ser Gly Phe Asp Phe Pro Ala Asp Val Asp Met Tyr Val Arg Ile Glu
115                  405                 410                 415
116  Phe Ser Val Tyr Val Gly Thr Leu Thr Leu Ala Ser Lys Ser Thr Thr
117              420                 425                 430
118  Lys Val Asn Ala Gln Phe Ala Lys Trp Asn Lys Glu Met Tyr Thr Phe
119          435                 440                 445
120  Asp Leu Tyr Met Lys Asp Met Pro Pro Ser Ala Val Leu Ser Ile Arg
121      450                 455                 460
122  Val Leu Tyr Gly Lys Val Lys Leu Lys Ser Glu Glu Phe Glu Val Gly
123  465                 470                 475                 480
124  Trp Val Asn Met Ser Leu Thr Asp Trp Arg Asp Glu Leu Arg Gln Gly
125                  485                 490                 495
126  Gln Phe Leu Phe His Leu Trp Ala Pro Glu Pro Thr Ala Asn Arg Ser
127              500                 505                 510
128  Arg Ile Gly Glu Asn Gly Ala Arg Ile Gly Thr Asn Ala Ala Val Thr
129          515                 520                 525
130  Ile Glu Ile Ser Ser Tyr Gly Gly Arg Val Arg Met Pro Ser Gln Gly
131      530                 535                 540
132  Gln Tyr Thr Tyr Leu Val Lys His Arg Ser Thr Trp Thr Glu Thr Leu
133  545                 550                 555                 560
134  Asn Ile Met Gly Asp Asp Tyr Glu Ser Cys Ile Arg Asp Pro Gly Tyr
135                  565                 570                 575
136  Lys Lys Leu Gln Met Leu Val Lys Lys His Glu Ser Gly Ile Val Leu
137              580                 585                 590
138  Glu Glu Asp Glu Gln Arg His Val Trp Met Trp Arg Arg Tyr Ile Gln
139          595                 600                 605
140  Lys Gln Glu Pro Asp Leu Leu Ile Val Leu Ser Glu Leu Ala Phe Val
141      610                 615                 620
142  Trp Thr Asp Arg Glu Asn Phe Ser Glu Leu Tyr Val Met Leu Glu Lys
143  625                 630                 635                 640
144  Trp Lys Pro Pro Ser Val Ala Ala Ala Leu Thr Leu Leu Gly Lys Arg
145                  645                 650                 655
146  Cys Thr Asp Arg Val Ile Arg Lys Phe Ala Val Glu Lys Leu Asn Glu
147              660                 665                 670
148  Gln Leu Ser Pro Val Thr Phe His Leu Phe Ile Leu Pro Leu Ile Gln
149          675                 680                 685
150  Ala Leu Lys Tyr Glu Pro Arg Ala Gln Ser Glu Val Gly Met Met Leu
151      690                 695                 700
152  Leu Thr Arg Ala Leu Cys Asp Tyr Arg Ile Gly His Arg Leu Phe Trp
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705                 710                 715                 720
Leu Leu Arg Ala Glu Ile Ala Arg Leu Arg Asp Cys Asp Leu Lys Ser
                725                 730                 735
Glu Glu Tyr Arg Arg Ile Ser Leu Leu Met Glu Ala Tyr Leu Arg Gly
            740                 745                 750
Asn Glu Glu His Ile Lys Ile Ile Thr Arg Gln Val Asp Met Val Asp
        755                 760                 765
Glu Leu Thr Arg Ile Ser Thr Leu Val Lys Gly Met Pro Lys Asp Val
    770                 775                 780
Ala Thr Met Lys Leu Arg Asp Glu Leu Arg Ser Ile Ser His Lys Met
785                 790                 795                 800
Glu Asn Met Asp Ser Pro Leu Asp Pro Val Tyr Lys Leu Gly Glu Met
                805                 810                 815
Ile Ile Asp Lys Ala Ile Val Leu Gly Ser Ala Lys Arg Pro Leu Met
            820                 825                 830
Leu His Trp Lys Asn Lys Asn Pro Lys Ser Asp Leu His Leu Pro Phe
        835                 840                 845
Cys Ala Met Ile Phe Lys Asn Gly Asp Asp Leu Arg Gln Asp Met Leu
    850                 855                 860
Val Leu Gln Val Leu Glu Val Met Asp Asn Ile Trp Lys Ala Ala Asn
865                 870                 875                 880
Ile Asp Cys Cys Leu Asn Pro Tyr Ala Val Leu Pro Met Gly Glu Met
                885                 890                 895
Ile Gly Ile Ile Glu Val Val Pro Asn Cys Lys Thr Ile Phe Glu Ile
            900                 905                 910
Gln Val Gly Thr Gly Phe Met Asn Thr Ala Val Arg Ser Ile Asp Pro
        915                 920                 925
Ser Phe Met Asn Lys Trp Ile Arg Lys Gln Cys Gly Ile Glu Asp Glu
    930                 935                 940
Lys Lys Lys Ser Lys Lys Asp Ser Thr Lys Asn Pro Ile Glu Lys Lys
945                 950                 955                 960
Ile Asp Asn Thr Gln Ala Met Lys Lys Tyr Phe Glu Ser Val Asp Arg
                965                 970                 975
Phe Leu Tyr Ser Cys Val Gly Tyr Ser Val Ala Thr Tyr Ile Met Gly
            980                 985                 990
Ile Lys Asp Arg His Ser Asp Asn Leu Met Leu Thr Glu Asp Gly Lys
        995                1000                1005
Tyr Val His Ile Asp Phe Gly His Ile Leu Gly His Gly Lys Thr Lys
   1010                1015                1020
Leu Gly Ile Gln Arg Asp Arg Gln Pro Phe Ile Leu Thr Glu His Phe
025                1030                1035                1040
Met Thr Val Ile Arg Ser Gly Lys Ser Val Asp Gly Asn Ser His Glu
               1045                1050                1055
Leu Gln Lys Phe Lys Thr Leu Cys Val Glu Ala Tyr Glu Val Met Trp
           1060                1065                1070
Asn Asn Arg Asp Leu Phe Val Ser Leu Phe Thr Leu Met Leu Gly Met
       1075                1080                1085
Glu Leu Pro Glu Leu Ser Thr Lys Ala Asp Leu Asp His Leu Lys Lys
   1090                1095                1100
Thr Leu Phe Cys Asn Gly Glu Ser Lys Glu Glu Ala Arg Lys Phe Phe
105                1110                1115                1120
Ala Gly Ile Tyr Glu Glu Ala Phe Asn Gly Ser Trp Ser Thr Lys Thr
               1125                1130                1135
```

Asn Trp Leu Phe His Ala Val Lys His Tyr
1140 1145

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGCCAT GGAGCTCGAG ATCTGATTGC TGGACACGGA CGGAACTCCG ACGTATCTCG 60
CAGATGCATG TTAACATTTT ACATCCACAA CTGCAAACGA TGGTCGAGCA GTGGCAAATG 120
CGAGAACGCC CATCGCTGGA GACCGAGAAT GGCAAAGGAT CGCTGCTCCT GGAAAATGAA 180
GGTGTCGCAG ATATCATCAC TATGTGTCCA TTCGGAGAAG TTATTAGTGT AGTATTTCCG 240
TGGTTTCTTG CAAATGTGCG AACATCGCTA GAAATCAAGC TATCAGATTT CAAACATCAA 300
CTTTTCGAAT TGATTGCTCC GATGAAGTGG GGAACATATT CCGTAAAGCC ACAGGATTAT 360
GTGTTCAGAC AGTTGAATAA TTTCGGCGAA ATTGAAGTTA TATTTAACGA CGATCAACCC 420
CTGTCGAAAT TAGAGCTCCA CGGCACTTTC CCAATGCTTT TTCTCTACCA ACCTGATGGA 480
ATAAACAGGG ATAAAGAATT AATGAGTGAT ATAAGTCATT GTCTAGGATA CTCACTGGAT 540
AAACTGGAAG AGAGCCTCGA TGAGGAACTC CGTCAATTTC GTGCTTCTCT CTGGGCTCGT 600
ACGAAGAAAA CGTGCTTGAC ACGTGGACTT GAGGGTACCA GTCACTACGC GTTCCCCGAA 660
GAACAGTACT TGTGTGTTGG TGAATCGTGC CCGAAAGATT TGGAATCAAA AGTCAAGGCT 720
GCCAAGCTGA GTTATCAGAT GTTTTGGAGA AAACGTAAAG CGGAAATCAA TGGAGTTTGC 780
GAGAAAATGA TGAAGATTCA AATTGAATTC AATCCGAACG AAACTCCGAA ATCTCTGCTT 840
CACACGTTTC TCTACGAAAT GCGAAAATTG GATGTATACG ATACCGATGA TCCTGCAGAT 900
GAAGGATGGT TTCTTCAATT GGCTGGACGT ACCACGTTTG TTACAAATCC AGATGTCAAA 960
CTTACGTCTT ATGATGGTGT CCGTTCGGAA CTGGAAAGCT ATCGATGCCC TGGATTCGTT 1020
GTTCGCCGAC AATCACTAGT CCTCAAAGAC TATTGTCGCC CAAAACCACT CTACGAACCA 1080
CATTATGTGA GAGCACACGA ACGAAAACTT GCTCTAGACG TGCTCAGCGT GTCTATAGAT 1140
AGCACACCAA AACAGAGCAA GAACAGTGAC ATGGTTATGA CTGATTTTCG TCCGACAGCT 1200
TCACTCAAAC AAGTTTCACT TTGGGACCTT GACGCGAATC TTATGATACG GCCTGTGAAT 1260
ATTTCTGGAT TCGATTTCCC GGCCGACGTG GATATGTACG TTCGAATCGA ATTCAGTGTA 1320
TATGTGGGGA CACTGACGCT GGCATCAAAA TCTACAACAA AAGTGAATGC TCAATTTGCA 1380
AAATGGAATA AGGAAATGTA CACTTTTGAT CTATACATGA AGGATATGCC ACCATCTGCA 1440
GTACTCAGCA TTCGTGTTTT GTACGGAAAA GTGAAATTAA AAAGTGAAGA ATTCGAAGTT 1500
GGTTGGGTAA ATATGTCCCT AACCGATTGG AGAGATGAAC TACGACAAGG ACAATTTTTA 1560
TTCCATCTGT GGGCTCCTGA ACCGACTGCC AATCGTAGTA GGATCGGAGA AAATGGAGCA 1620
AGGATAGGCA CCAACGCAGC GGTTACAATT GAAATCTCAA GTTATGGTGG TAGAGTTCGA 1680
ATGCCGAGTC AAGGACAATA CACATATCTC GTCAAGCACC GAAGTACTTG GACGGAAACT 1740
TTGAATATTA TGGGTGATGA CTATGAGTCG TGTATCAGAG ATCCAGGATA TAAGAAGCTT 1800
CAGATGCTTG TCAAGAAGCA TGAATCTGGA ATTGTATTAG AGGAAGATGA ACAACGTCAT 1860
GTCTGGATGT GGAGGAGATA CATTCAAAAG CAGGAGCCTG ATTTGCTCAT TGTGCTCTCC 1920
GAACTCGCAT TTGTGTGGAC TGATCGTGAG AACTTTTCCG AGCTCTATGT GATGCTTGAA 1980
AAATGGAAAC CGCCGAGTGT GGCAGCCGCG TTGACTTTGC TTGGAAAACG TTGCACGGAT 2040
CGTGTGATTC GAAAGTTTGC AGTGGAGAAG TTGAATGAGC AGCTGAGCCC GGTCACATTC 2100
CATCTTTTCA TATTGCCTCT CATACAGGCG TTGAAGTACG AACCGCGTGC TCAATCGGAA 2160
GTTGGAATGA TGCTCTTGAC TAGAGCTCTC TGCGATTATC GAATTGGACA TCGACTTTTC 2220
TGGCTGCTCC GTGCAGAGAT TGCTCGTTTG AGAGATTGTG ATCTGAAAAG TGAAGAATAT 2280

**SEQUENCE VERIFICATION REPORT**
PATENT APPLICATION ***US/08/908,453***

DATE: 10/22/98
TIME: 09:36:32

***INPUT SET: S29199.raw***

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